



SYR-HDAC-5005-U sub seq list 2.ST25
SEQUENCE LISTING

<110> Syrrx, Inc.
<120> HISTONE DEACETYLASE INHIBITORS
<130> SYR-HDAC-5005-U
<140> US 10/803,344
<141> 2004-03-17
<150> US 60/455,437
<151> 2003-03-17
<150> US 60/531,203
<151> 2003-12-19
<160> 8
<170> PatentIn version 3.2
<210> 1
<211> 513
<212> PRT
<213> Artificial
<220>
<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHDYDIPPTENLYFQGAMEPGGS" tag at the N-terminus
<400> 1

Met Ser Tyr Tyr His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
35 40 45

Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
50 55 60

Arg Ile Arg Met Thr His Asn Leu Leu Asn Tyr Gly Leu Tyr Arg
65 70 75 80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
115 120 125

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Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
130 135 140

Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
145 150 155 160

Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
165 170 175

Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
180 185 190

Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
195 200 205

His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
210 215 220

Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
225 230 235 240

Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
245 250 255

Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
260 265 270

Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
275 280 285

Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
290 295 300

Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
305 310 315 320

Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr Ile
325 330 335

Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
340 345 350

Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
355 360 365

Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
370 375 380

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Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
 385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
 405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
 420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
 435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys Asn
 450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
 465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
 485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
 500 505 510

Ala

<210> 2
 <211> 1542
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence encoding residues 1-482 of HDAC1 with a
 "MSYYHHHHHDYDIPPTTENLYFQGAMEPGGS" tag at the N-terminus

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tattttcagg ggcgcattgga acccgggggga tccatggcgc agacgcaggc caccggagg	120	
aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca	180	
atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga	240	
aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc	300	
gatgactaca ttaaattctt ggcgtccatc cgtccagata acatgtcggc gtacagcaag	360	
cagatgcaga gattcaacgt tggtgaggac tgtccagat tcgatggcct gtttgagttc	420	
tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg	480	

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gacatcgctg tgaattgggc tggggccctg caccatgcaa agaagtccga ggcacatctggc	540
ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg	600
gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaaagaggc cttctacacc	660
acggaccggg tcatgactgt gtccttcat aagtatggag agtacttccc aggaactggg	720
gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga	780
gacgggattg atgacgagtc ctatgaggcc atttcaagc cggtcatgtc caaagtaatg	840
gagatgttcc agcctagtgc ggtggctta cagtgtggct cagactccct atctggggat	900
cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgcgtcaag	960
agctttaacc tgcctatgtc gatgctggga ggcggtggtt acaccattcg taacgttgcc	1020
cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca	1080
tacaatgact actttgaata ctggacca gatttcaagc tccacatcag tccttccaat	1140
atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac	1200
cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc	1260
cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcacatc gatctgctcc	1320
tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg	1380
ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaaa	1440
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<210> 3

<211> 498

<212> PRT

<213> Artificial

<220>

<223> Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 3

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1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
50 55 60

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Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
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305 310 315 320
SYR-HDAC-5005-U sub seq list 2.ST25
Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
325 330 335
Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
340 345 350
Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
355 360 365
Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
370 375 380
Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
385 390 395 400
Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
405 410 415
Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
420 425 430
Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
435 440 445
Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
450 455 460
Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
465 470 475 480
Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
485 490 495
His His

<210> 4
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4
atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaaaa aagtctgcta ctactacgac 60

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atgaccata	acttgctgtt	aaattatggc	ttatacagaa	aatggaaat	atataggccc	180
cataaagcca	ctgccgaaga	aatgacaaaa	tatcacagt	atgagtatat	caaattctca	240
cggtaataa	gaccagataa	catgtcttag	tatagtaagc	agatgcagag	attnaatgtt	300
ggagaagatt	gtccagtgtt	tatggactc	tttgagttt	gtcagctctc	aactggcggt	360
tcagttgctg	gagctgtgaa	gttaaaccga	caacagactg	atatggctgt	taattgggct	420
ggaggattac	atcatgctaa	gaaatcagaa	gcatcaggat	tctgttacgt	taatgatatt	480
gtgcttgcca	tccttgaatt	actaaagtat	catcagagag	tcttatatat	tgatatacat	540
attcatcatg	gtgatggtgt	tgaagaagct	ttttatacaa	cagatcgtgt	aatgacggta	600
tcattccata	aatatgggaa	atacttcct	ggcacaggag	acttgaggga	tattggtgct	660
ggaaaaggca	aatactatgc	tgtcaatttt	ccaatgagag	atggtataga	tgatgagtca	720
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gtggtattac	agtgtggtgc	agactcatta	tctggtata	gactgggttg	tttcaatcta	840
acagtcaaag	gtcatgctaa	atgtgtagaa	gttgaaaaaa	cttttaactt	accattactg	900
atgcttgag	gaggtggcta	cacaatccgt	aatgttgc	gatgtggac	atatgagact	960
gcagttgccc	ttgattgtga	gattccaat	gagttccat	ataatgatta	ctttgagtat	1020
tttggaccag	acttcaaact	gcatattagt	ccttcaaaca	tgacaaacca	gaacactcca	1080
gaatatatgg	aaaagataaa	acagcgttt	tttggaaatt	tgcgcatttt	acctcatgca	1140
cctgggtgtcc	agatgcaagc	tattccagaa	gatgctgttc	atgaagacag	tggagatgaa	1200
gatggagaag	atccagacaa	gagaatttct	attcgagcat	cagacaagcg	gatagctgt	1260
gatgaagaat	tctcagattc	tgaggatgaa	ggagaaggag	gtcgaagaaa	tgtggctgat	1320
cataagaaag	gagcaaagaa	agctagaatt	gaagaagata	agaaagaaac	agaggacaaa	1380
aaaacagacg	ttaaggaaga	agataaatcc	aaggacaaca	gtggtaaaaa	aacagatacc	1440
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<210> 5
<211> 782
<212> PRT
<213> Artificial

<220>
<223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus
and a "MP" tag at the N-terminus

<400> 5

Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr
1 5 10 15

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Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
20 25 30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
35 40 45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
50 55 60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
65 70 75 80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
85 90 95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser
100 105 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val
115 120 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly
130 135 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His
145 150 155 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg
165 170 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe
180 185 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr
195 200 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr
210 215 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn
225 230 235 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val
245 250 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala
260 265 270

SYR-HDAC-5005-U sub seq list 2.ST25

Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
275 280 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
290 295 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305 310 315 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
325 330 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
340 345 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
355 360 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
370 375 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385 390 395 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
405 410 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
420 425 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
435 440 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
450 455 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465 470 475 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
485 490 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
500 505 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
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515 520 525

Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540 545 550 555 560
Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
565 570 575
Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
580 585 590
Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
595 600 605
Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620
Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640
Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655
Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670
Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685
Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700
Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720
Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735
Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750
Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

SYR-HDAC-5005-U sub seq list 2.ST25
 Val Glu Asp Arg Glu Gly Pro Gly His His His His His His His
 770 775 780

<210> 6
 <211> 2349
 <212> DNA
 <213> Artificial

<220>
 <223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

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 cggctccatg ccatcaagga gcaactgatc caggagggcc tcctagatcg ctgcgtgtcc 180
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 gatctgatgg aaacaaccca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300
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 aactggtcca ccacaggtt cggccaaggc caaggatata ccatcaatgt gccttggAAC 720
 caggtggggta tgcggatgc tgactacatt gctgcttcc tgacgtcct gctgccagtc 780
 gcccctcgagt tccagcctca gctggcctcg gtggctgctg gatttgcgtgc cctgcaaggg 840
 gaccccaagg gtgagatggc cgccactccg gcagggttcg cccagctaac ccacctgctc 900
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 cttgagccct tctgggaggt tcttgtgaga tcaactgaga ccgtggagag ggacaacatg 1140
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 atcctgacat ggccagtgc acagtctcgc acagggtgg tctatgacca aaatatgatg 1260
 aatcactgca acttgtggaa cagccaccac cctgaggtac cccagcgcat cttgcggatc 1320
 atgtgccgtc tggaggagct gggccttgcc gggcgctgcc tcaccctgac accgcgccct 1380
 gcccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccggGCC 1440
 acagagaaaa tgaaaacccg ggagctgcac cgtgagagtt ccaactttga ctccatctat 1500

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gaggctgtgc	tctcaggaga	ggttctgaat	ggtgctgctg	tggtgcgatcc	cccaggacac	1620
cacgcagagc	aggatgcagc	ttgcggttt	tgctttca	actctgtggc	tgtggctgct	1680
cgccatgccc	agactatcag	tgggcatgcc	ctacggatcc	tgattgtgga	ttgggatgtc	1740
caccacggta	atggaactca	gcacatgttt	gaggatgacc	ccagtgtgct	atatgtgtcc	1800
ctgcaccgct	atgatcatgg	caccccttc	cccatggggg	atgagggtgc	cagcagccag	1860
atcggccggg	ctgcgggcac	aggcttcacc	gtcaacgtgg	catggAACGG	gccccgcatt	1920
gggtatgctg	actacctagc	tgcctggcat	cgcctggtg	ttcccattgc	ctacgagttt	1980
aaccacaaac	ttggtgcgtgt	ctcagctggc	tttgatgctg	cacgggggg	tccgctgggg	2040
ggctgccagg	tgtcacctga	gggttatgcc	cacccacccc	acctgctgat	gggccttgcc	2100
agtggccgca	ttatccttat	cctagagggt	ggctataacc	tgacatccat	ctcagagtcc	2160
atggctgcct	gcactcgctc	cctccttgga	gaccaccac	ccctgctgac	cctgccacgg	2220
ccccactat	cagggccct	ggcctaattc	actgagacca	tccaaagtcca	tcgcagatac	2280
tggcgagct	tacgggtcat	gaaggtagaa	gacagagaag	gaccgggca	tcaccatcac	2340
catcaactaa						2349

<210> 7
 <211> 385
 <212> PRT
 <213> Artificial

<220>
 <223> Residues 1-377 of HDAC8 with a "MHHHHHHHP" tag at the N-terminus
 <400> 7

Met His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala
 1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
 20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
 35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
 50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
 65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp
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SYR-HDAC-5005-U sub seq list 2. ST25
90 95Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300Ala Thr Leu Ile Leu Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

SYR-HDAC-5005-U sub seq list 2.ST25
Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
370 375 380

Val
385

<210> 8
<211> 1158
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 1-377 of HDAC8 with a "MHHHHHHHP" tag at the N-terminus

<400> 8
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gatcatgagt tttcacagc atatggcct gattatgtgc tggaaatcac gccaagctgc 1080
cggccagacc gcaatgagcc ccaccgaatc caacaaatcc tcaactacat caaaggaaat 1140

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ctgaagcatg tggtag

1158



SYR-HDAC-5005-U sub seq list 2.ST25
SEQUENCE LISTING

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<141> 2004-03-17
<150> US 60/455,437
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<150> US 60/531,203
<151> 2003-12-19
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<170> PatentIn version 3.2
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<211> 513
<212> PRT
<213> Artificial
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<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus
<400> 1

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Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp Gly
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Asp Val Gly Asn Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
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Arg Ile Arg Met Thr His Asn Leu Leu Asn Tyr Gly Leu Tyr Arg
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Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
115 120 125

SYR-HDAC-5005-U sub seq list 2.ST25

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145 150 155 160

Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
165 170 175

Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
180 185 190

Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
195 200 205

His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
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Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
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Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
260 265 270

Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
275 280 285

Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
290 295 300

Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
305 310 315 320

Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr Ile
325 330 335

Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
340 345 350

Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
355 360 365

Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
370 375 380

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Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
 385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
 405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
 420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
 435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys Asn
 450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
 465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
 485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
 500 505 510

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<210> 2
 <211> 1542
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence encoding residues 1-482 of HDAC1 with a
 "MSYYHHHHHDYDIPPTTENLYFQGAMEPGGS" tag at the N-terminus

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 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca 180
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 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300
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 cagatgcaga gattcaacgt tggtgaggac tgtccagtt tcgatggcct gtttgagttc 420
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gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaaagaggc cttctacacc	660
acggaccggg tcatgactgt gtccttcat aagtatggag agtacttccc aggaactggg	720
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<210> 3

<211> 498

<212> PRT

<213> Artificial

<220>

<223> Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 3

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1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
50 55 60

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Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
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310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
420 425 430

Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
435 440 445

Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
450 455 460

Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
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Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
485 490 495

His His

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<210> 4
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4
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SYR-HDAC-5005-U sub seq list 2.ST25

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aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtaaaaa aacagatacc	1440
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 <211> 782
 <212> PRT
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 <223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus
 and a "MP" tag at the N-terminus

<400> 5

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 1 5 10 15

SYR-HDAC-5005-U sub seq list 2.ST25

Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
20 25 30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
35 40 45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
50 55 60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
65 70 75 80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
85 90 95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser
100 105 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val
115 120 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly
130 135 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His
145 150 155 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg
165 170 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe
180 185 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr
195 200 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr
210 215 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn
225 230 235 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val
245 250 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala
260 265 270

SYR-HDAC-5005-U sub seq list 2.ST25

Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
275 280 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
290 295 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305 310 315 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
325 330 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
340 345 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
355 360 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
370 375 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385 390 395 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
405 410 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
420 425 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
435 440 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
450 455 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465 470 475 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
485 490 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
500 505 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
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Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540 545 550 555 560

Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
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Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
565 570 575

Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
580 585 590

Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr
595 600 605

Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620

Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640

Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655

Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670

Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685

Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700

Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720

Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735

Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750

Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

SYR-HDAC-5005-U sub seq list 2.ST25
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770 775 780

<210> 6
<211> 2349
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

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gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccggGCC 1440
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SYR-HDAC-5005-U sub seq list 2.ST25

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catcaactaa						2349

<210> 7
 <211> 385
 <212> PRT
 <213> Artificial

<220>
 <223> Residues 1-377 of HDAC8 with a "MHHHHHHHP" tag at the N-terminus
 <400> 7

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 1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
 20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
 35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
 50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
 65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp
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85

90

95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
 100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
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Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
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Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
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Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
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Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
 180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
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His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
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Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
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Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
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Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
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Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
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Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
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Ala Thr Leu Ile Leu Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
 305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
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Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
 340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
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Val
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 aagatccccca aacgggccag tatggtgc tctttgattt aagcatatgc actgcataag 180
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1158